

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/ 531, 479  
Source: PST  
Date Processed by STIC: 4-25-05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 04/25/2005

PATENT APPLICATION: US/10/531,479

TIME: 12:24:32

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04252005\J531479.raw

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5 <110> APPLICANT: VIB vzw
9 <120> TITLE OF INVENTION: A role in lignification and growth for plant phenylcoumaran
benzylic
10 ether reductase
14 <130> FILE REFERENCE: WBO/PCBER/V130
C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/531,479
C--> 18 <141> CURRENT FILING DATE: 2005-04-15
18 <150> PRIOR APPLICATION NUMBER: EP 02079407.9
20 <151> PRIOR FILING DATE: 2002-10-18
24 <160> NUMBER OF SEQ ID NOS: 2
28 <170> SOFTWARE: PatentIn version 3.1
32 <210> SEQ ID NO: 1
34 <211> LENGTH: 1199
36 <212> TYPE: DNA
38 <213> ORGANISM: Populus balsamifera subsp. trichocarpa
42 <220> FEATURE:
44 <221> NAME/KEY: CDS
46 <222> LOCATION: (51)..(977)
48 <223> OTHER INFORMATION:
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53 gcaacgagggtt aaacttcctt gggtttctttc atcaagaaaa attatctaca atg gct 56
54 Met Ala
55 1
57 gat aaa agc aaa atc ttg atc att gga ggt act ggt tac ata gga aaa 104
58 Asp Lys Ser Lys Ile Leu Ile Ile Gly Gly Thr Gly Tyr Ile Gly Lys
59 5 10 15
61 ttc atc gtg gag gca agc gcc aag gcc ggt cac ccc act ttc gcc ttg 152
62 Phe Ile Val Glu Ala Ser Ala Lys Ala Gly His Pro Thr Phe Ala Leu
63 20 25 30
65 gtt aga gag agt aca gtc tct gat cct gtc aaa cga gaa ctt gtc gag 200
66 Val Arg Glu Ser Thr Val Ser Asp Pro Val Lys Arg Glu Leu Val Glu
67 35 40 45 50
69 aaa ttc aag aac tta ggc gtc act ttg atc cat gga gat gtc gac ggc 248
70 Lys Phe Lys Asn Leu Gly Val Thr Leu Ile His Gly Asp Val Asp Gly
71 55 60 65
73 cat gac aat ttg gtg aag gca atc aag cgg gtg gat gtg gtg ata tca 296
74 His Asp Asn Leu Val Lys Ala Ile Lys Arg Val Asp Val Val Ile Ser
75 70 75 80
77 gcg att ggg agc atg caa ata gca gat caa acc aag atc att gcc gcc 344
78 Ala Ile Gly Ser Met Gln Ile Ala Asp Gln Thr Lys Ile Ile Ala Ala
79 85 90 95
81 att aaa gaa gct ggc aat gtc aag aga ttc ttc cct tca gaa ttt gga 392
82 Ile Lys Glu Ala Gly Asn Val Lys Arg Phe Phe Pro Ser Glu Phe Gly
83 100 105 110

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85 atg gat gtg gat cat gtc aat gct gtt gag cct gca aaa act gca ttt      440
86 Met Asp Val Asp His Val Asn Ala Val Glu Pro Ala Lys Thr Ala Phe
87 115                               120                               125                               130
89 gca atg aag gct cag att cga cgt gcc atc gag gct gca ggg att ccc      488
90 Ala Met Lys Ala Gln Ile Arg Arg Ala Ile Glu Ala Ala Gly Ile Pro
91                               135                               140                               145
93 tac act tat gtg cct tcc aac ttc ttt gct gca tat tat ctc ccc aca      536
94 Tyr Thr Tyr Val Pro Ser Asn Phe Phe Ala Ala Tyr Tyr Leu Pro Thr
95                               150                               155                               160
97 ttg gca cag ttt gga ctt act gct cct ccg aga gac aag atc acc atc      584
98 Leu Ala Gln Phe Gly Leu Thr Ala Pro Pro Arg Asp Lys Ile Thr Ile
99                               165                               170                               175
101 ctc gga gat ggc aat gcc aag ttg gtt ttc aat aag gaa gat gac att      632
102 Leu Gly Asp Gly Asn Ala Lys Leu Val Phe Asn Lys Glu Asp Asp Ile
103 180                               185                               190
105 gga acc tac acc atc aaa gct gtg gat gat gca aga acc ttg aac aag      680
106 Gly Thr Tyr Thr Ile Lys Ala Val Asp Asp Ala Arg Thr Leu Asn Lys
107 195                               200                               205                               210
109 act gtc cta atc aag cct cct aaa aac acc tac tca ttc aat gag ctt      728
110 Thr Val Leu Ile Lys Pro Pro Lys Asn Thr Tyr Ser Phe Asn Glu Leu
111                               215                               220                               225
113 att gat cta tgg gag aaa aag att ggc aaa acc ctc gaa aaa acc ttt      776
114 Ile Asp Leu Trp Glu Lys Lys Ile Gly Lys Thr Leu Glu Lys Thr Phe
115                               230                               235                               240
117 gtt cct gaa gag aaa ctt ctg aag gac atc caa gag tct ccg att ccg      824
118 Val Pro Glu Glu Lys Leu Leu Lys Asp Ile Gln Glu Ser Pro Ile Pro
119                               245                               250                               255
121 att aat att gtt ctg tca atc aac cac tca gcc ctc gtt aat ggt gac      872
122 Ile Asn Ile Val Leu Ser Ile Asn His Ser Ala Leu Val Asn Gly Asp
123 260                               265                               270
125 atg acc aac ttt gag att gac cca tca tgg ggc ctt gag gcc tct gag      920
126 Met Thr Asn Phe Glu Ile Asp Pro Ser Trp Gly Leu Glu Ala Ser Glu
127 275                               280                               285                               290
129 cta tat cca gat gtc aaa tat acc acc gtg gaa gag tac ctt gat cag      968
130 Leu Tyr Pro Asp Val Lys Tyr Thr Thr Val Glu Glu Tyr Leu Asp Gln
131                               295                               300                               305
133 ttt gtc tga ggcactggca tctcctgctc tccagttatt aatgaaacaa      1017
134 Phe Val
137 acagccgaat agttggaaat ttgggtgttt cttatagacg agtggttgtc caagtcaagg      1077
139 aggtctcttt ccttataaac ctgtgaaat gatgttctgc tctagttaat tgccatggtt      1137
141 tgtatctatt gctggaagag atgttctggg tgagaataat gtaattgagt tatgatgaat      1197
143 aa
146 <210> SEQ ID NO: 2
148 <211> LENGTH: 308
150 <212> TYPE: PRT
152 <213> ORGANISM: Populus balsamifera subsp. trichocarpa
156 <400> SEQUENCE: 2
158 Met Ala Asp Lys Ser Lys Ile Leu Ile Ile Gly Gly Thr Gly Tyr Ile
159 1                               5                               10                               15

```

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```

162 Gly Lys Phe Ile Val Glu Ala Ser Ala Lys Ala Gly His Pro Thr Phe
163      20      25      30
166 Ala Leu Val Arg Glu Ser Thr Val Ser Asp Pro Val Lys Arg Glu Leu
167      35      40      45
170 Val Glu Lys Phe Lys Asn Leu Gly Val Thr Leu Ile His Gly Asp Val
171      50      55      60
174 Asp Gly His Asp Asn Leu Val Lys Ala Ile Lys Arg Val Asp Val Val
175 65      70      75      80
178 Ile Ser Ala Ile Gly Ser Met Gln Ile Ala Asp Gln Thr Lys Ile Ile
179      85      90      95
182 Ala Ala Ile Lys Glu Ala Gly Asn Val Lys Arg Phe Phe Pro Ser Glu
183      100     105     110
186 Phe Gly Met Asp Val Asp His Val Asn Ala Val Glu Pro Ala Lys Thr
187      115     120     125
190 Ala Phe Ala Met Lys Ala Gln Ile Arg Arg Ala Ile Glu Ala Ala Gly
191      130     135     140
194 Ile Pro Tyr Thr Tyr Val Pro Ser Asn Phe Phe Ala Ala Tyr Tyr Leu
195 145     150     155     160
198 Pro Thr Leu Ala Gln Phe Gly Leu Thr Ala Pro Pro Arg Asp Lys Ile
199      165     170     175
202 Thr Ile Leu Gly Asp Gly Asn Ala Lys Leu Val Phe Asn Lys Glu Asp
203      180     185     190
206 Asp Ile Gly Thr Tyr Thr Ile Lys Ala Val Asp Asp Ala Arg Thr Leu
207      195     200     205
210 Asn Lys Thr Val Leu Ile Lys Pro Pro Lys Asn Thr Tyr Ser Phe Asn
211      210     215     220
214 Glu Leu Ile Asp Leu Trp Glu Lys Lys Ile Gly Lys Thr Leu Glu Lys
215 225     230     235     240
218 Thr Phe Val Pro Glu Glu Lys Leu Leu Lys Asp Ile Gln Glu Ser Pro
219      245     250     255
222 Ile Pro Ile Asn Ile Val Leu Ser Ile Asn His Ser Ala Leu Val Asn
223      260     265     270
226 Gly Asp Met Thr Asn Phe Glu Ile Asp Pro Ser Trp Gly Leu Glu Ala
227      275     280     285
230 Ser Glu Leu Tyr Pro Asp Val Lys Tyr Thr Thr Val Glu Glu Tyr Leu
231      290     295     300
234 Asp Gln Phe Val
235 305

```

VERIFICATION SUMMARY

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L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:52 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:48